

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:20:13 ; Search time 52.2 Seconds
(without alignments)
28.617 Million cell updates/sec

Title: US-09-331-631a-39

Perfect score: 34

Sequence: 1 CXXXCXXXXXXXXXXXXCXXXC 22

Scoring table:

BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 6790655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR66:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	40	1 SMFP	metallothionein Mt
2	54	100.0	40	2 B61194	metallothionein 1B
3	54	100.0	43	1 SMFE2	metallothionein 2
4	54	100.0	44	2 I48945	cellular disintegr
5	54	100.0	44	2 I48942	cellular disintegr
6	54	100.0	46	2 I48947	cellular disintegr
7	54	100.0	47	2 JC5557	arginine/glutamate
8	54	100.0	52	2 S65712	metallothionein 1
9	54	100.0	53	2 S01179	hypothetical prote
10	54	100.0	55	2 S25774	testis-specific pr
11	54	100.0	57	1 SMK2D5	metallothionein 2
12	54	100.0	57	1 S59073	metallothionein 1
13	54	100.0	58	1 SMK2D5	metallothionein 1
14	54	100.0	58	1 S59072	metallothionein 1
15	54	100.0	58	2 A37039	metallothionein 1
16	54	100.0	58	2 S43367	metallothionein 1
17	54	100.0	61	1 SMH01B	metallothionein 1B
18	54	100.0	63	2 S25772	testis-specific pr
19	54	100.0	64	2 A25775	metallothionein A
20	54	100.0	64	2 A33825	metallothionein A
21	54	100.0	66	2 S36866	metallothionein -
22	54	100.0	66	2 S59621	metallothionein is
23	54	100.0	67	2 T11547	metallothionein -
24	54	100.0	68	2 S25775	testis-specific pr
25	54	100.0	68	2 S07807	WDNM1 protein - ra
26	54	100.0	71	2 S47576	metallothionein 20
27	54	100.0	71	2 S47577	metallothionein 20
28	54	100.0	71	2 S39420	metallothionein 20
29	54	100.0	71	2 S39422	metallothionein 20

30	54	100.0	71	2 S39421	metallothionein 20
31	54	100.0	74	2 S25773	testis-specific pr
32	54	100.0	74	2 S61553	probable proteins
33	54	100.0	75	2 S17156	metallothionein -
34	54	100.0	75	2 T21519	hypothetical prote
35	54	100.0	76	2 T09262	glycine-rich cell
36	54	100.0	76	2 T03860	hypothetical prote
37	54	100.0	86	2 T25303	TA20 protein - com
38	54	100.0	87	2 T00564	hypothetical prote
39	54	100.0	90	2 T25304	hypothetical prote
40	54	100.0	93	2 JE0159	giberellin-stimul
41	54	100.0	95	2 T06275	benzothiadiazole-1
42	54	100.0	95	2 T15330	hypothetical prote
43	54	100.0	96	2 S43910	giberellin-regula
44	54	100.0	97	2 S71371	giberellin-regula
45	54	100.0	98	2 S60229	giberellin-regula

ALIGNMENTS

RESULT 1

SMFP
metallothionein Mtn - fruit fly (Drosophila melanogaster)

N:Alternate names: MT

C:Species: Drosophila melanogaster

C>Date: 17-Mar-1987 #sequence-revision 17-Mar-1987 #text_change 22-Jun-1999

C:Accession: A25294; A03285; A48734; A61194

R:Maroni, G.; Otto, E.; Lastowski-Perry, D.

Genetics 112, 493-504, 1986

A:Title: Molecular and cytogenetic characterization of a metallothionein gene of Dros

A:Reference number: A25294; MUID:86165787

A:Accession: A25294

A:Molecule type: DNA

A:Residues: 1-40 <MAR>

A:Cross-references: GB:X03758; GB:M12964; NID:98272; PIDN:CAA27391.1; PID:98273

R:Lastowski-Perry, D.; Otto, E.; Maroni, G.

J. Biol. Chem. 260, 1527-1530, 1985

A:Title: Nucleotide sequence and expression of a Drosophila metallothionein.

A:Reference number: A03285; MUID:85105016

A:Accession: A03285

A:Molecule type: mRNA

A:Residues: 1-40 <LAS>

A:Cross-references: GB:K02314; GB:M35390; NID:9157876; PIDN:AAA28681.1; PID:9157877

A:Experimental source: Samarkand stock, larva

A:Note: this allele is designated Mtn-1

R:Maroni, G.; Lastowski-Perry, D.; Otto, E.; Watson, D.

Environ. Health Perspect. 65, 107-116, 1986

A:Title: Effects of heavy metals on Drosophila larvae and a metallothionein cDNA.

A:Reference number: A48734; MUID:86219988

A:Accession: A48734

A:Molecule type: mRNA

A:Residues: 1-40 <MA2>

A:Cross-references: GB:K02314; NID:9157876; PIDN:AAA28681.1; PID:9157877

R:Theodore, L.; Ho, A.S.; Maroni, G.

Genet. Res. 58, 203-210, 1991

A:Title: Recent evolutionary history of the metallothionein gene Mtn in Drosophila.

A:Reference number: A61194; MUID:92201681

A:Accession: A61194

A:Molecule type: DNA

A:Residues: 1-39, 'K' <THE>

A:Cross-references: GB:M69015; NID:9157915; PIDN:AA841334.1; PID:9157916

A:Note: this allele is designated Mtn-3

C:Comment: This protein binds cations of several transition elements.

C:Comment: All cysteine residues are arranged in C-X-C groups. These are thought to b

C:Genetics:

A:Gene: Mtn

A:Cross-references: FlyBase:FBgn0002868

A:Map position: 3R 85E10-15

A:Introns: 8/1

A:Note: Several alleles of Mtn are known; the metallothionein gene Mtn is very distan

C:Superfamily: metallothionein

C:Keywords: chelation; metal binding

RESULT 6
148947
cellular disintegrin-related protein 40 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 20-Sep-1999
C:Accession: I48947
R:Meskamp, G.; Blobel, C.P.
Proc. Natl. Acad. Sci. U.S.A. 91, 2748-2751, 1994
A:Title: A new family of cellular proteins related to snake venom disintegrins.
A:Reference number: A53476; MUID:94195820
A:Accession: I48947
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-46 <RES>
A:Cross-references: EMBL:U06149; NID:9487146; PIDN:AAA18428.1; PID:9487147
C:Superfamily: unassigned disintegrins; disintegrin homology

Query Match 100.0%; Score 54; DB 2; Length 46;
Best Local Similarity 18.2%; Pred. No. 1.5e+02;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 22
|::|::|::|::|::|::|::|::|
Db 11 CSSDCVLKPCACAFGLCKNC 32

RESULT 7
JC5557
arginine/glutamate-rich 6.5K polypeptide - smooth loofah
C:Species: Luffa cylindrica (smooth loofah)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 07-May-1999
C:Accession: JC5557
R:Kimura, M.; Park, S.S.; Sakai, R.; Yamasaki, N.; Funatsu, G.
Biochem. Biotechnol. Biochem. 61, 984-988, 1997
A:Title: Primary structure of 6.5K-arginine/glutamate-rich polypeptide from the seeds of
A:Reference number: JC5557; MUID:97357433
A:Accession: JC5557
A:Molecule type: protein
A:Residues: 1-47 <KIM>
A:Experimental source: seed
C:Comment: This protein is a storage protein which provides nitrogen and carbon reserves
F/12-33,16-29/disulfide bonds: #status predicted

Query Match 100.0%; Score 54; DB 2; Length 47;
Best Local Similarity 18.2%; Pred. No. 1.5e+02;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 22
|::|::|::|::|::|::|::|::|
Db 12 CRVRCQVAHEGVERKRCQVC 33

RESULT 8
S65712
metallothionein 1 - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
C:Accession: S65712
R:Saito, S.; Hunziker, P.E.
Biochim. Biophys. Acta 1289, 65-70, 1996
A:Title: Differential sensitivity of metallothionein-1 and -2 in liver of zinc-injected
A:Reference number: S65712; MUID:96195842
A:Accession: S65712
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23; 24-46; 47-52 <SAT>
C:Superfamily: metallothionein
C:Keywords: blocked amino end

Query Match 100.0%; Score 54; DB 2; Length 52;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 22
|::|::|::|::|::|::|::|::|
Db 13 CSSSCGCKNCKKSCCSCPCVC 34

RESULT 9
S01179
hypothetical protein P-5 - Chlamydia trachomatis plasmid pLGV440
C:Species: Chlamydia trachomatis
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 18-Jun-1993
C:Accession: S01179
R:Hatt, C.; Ward, M.E.; Clarke, I.N.
Nucleic Acids Res. 16, 4053-4067, 1988
A:Title: Analysis of the entire nucleotide sequence of the cryptic plasmid of Chlamyd
A:Reference number: S00788; MUID:88233998
A:Accession: S01179
A:Molecule type: DNA
A:Residues: 1-53 <HAT>
A:Cross-references: EMBL:X06707
C:Genetics:
A:Genome: plasmid

Query Match 100.0%; Score 54; DB 2; Length 53;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 22
|::|::|::|::|::|::|::|::|
Db 13 CNDACKCIPIKKNALPKCIKVC 34

RESULT 10
S25774
testis-specific protein Mst84Dc - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
C:Accession: S25774; C56565
R:Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991
A:Title: A cluster of four genes selectively expressed in the male germ line of Droso
A:Reference number: A56565; MUID:92102953
A:Accession: S25774
A:Molecule type: DNA
A:Residues: 1-55 <RUH>
A:Cross-references: EMBL:X67703; NID:911072; PIDN:CAA47939.1; PID:911075
A:Note: the authors translated the codon TGC for residue 55 as Thr
A:Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIT:74222)
C:Genetics:
A:Gene: Mst84Dc
A:Cross-references: FlyBase:FBgn0004174
A:Map position: 3
C:Superfamily: fruit fly testis-specific protein
C:Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 54; DB 2; Length 55;
Best Local Similarity 18.2%; Pred. No. 1.6e+02;
Matches 4; Conservative 18; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXCXXXXXXXXXXCXXC 22
|::|::|::|::|::|::|::|::|
Db 15 CGPCGCGPCRCGCGSCGCP 36

RESULT 11
SMKD25
metallothionein 2 - mud crab

